

SEQUENCE LISTING

<110> CHUGAI SEIYAKU KABUSHIKI KAISHA

<120> Method of stabilizing protein solutions

<130> C1-A0319P

<150> JP 2003-351410

<151> 2003-10-09

<160> 18

<170> PatentIn version 3.1

<210> 1

<211> 1779

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1779)

<223>

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1 5 10 15

gtc cag tgt gag gtg cag ctg ttg gat tct ggg gga ggc ttg gta cag 96  
Val Gln Cys Glu Val Gln Leu Leu Asp Ser Gly Gly Gly Leu Val Gln  
20 25 30

cct ggg ggg tgc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttt 144  
Pro Gly Gly Cys Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe  
35 40 45

agc agc tgt gcc atg agc tgg gtc cgc cag gct cca ggg aag ggg ctg 192  
 Ser Ser Cys Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu  
 50 55 60

gag tgg gtc tca gct att agt ggt agt ggt ggt agc aca tac tac gca 240  
Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala  
65 70 75 80

gac tcc gtg aag ggC cgg ttc acc atc tcc aga gac aaa tcc aag aac 288  
Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Lys Ser Lys Asn  
85 90 95

acg ttg tat ctg caa atg aac agc ctg aga gcc gag gac acg gcc gta 336  
Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val  
100 105 110

tat tac tgt gcg aaa ggt ggc aac gat att ttg act ggt tat tat gct 384  
Tyr Tyr Cys Ala Lys Gly Gly Asn Asp Ile Leu Thr Gly Tyr Tyr Ala  
115 120 125

tgg ggc cag gga acc ctg gtc acc gtc tcc tca ggg agt gca tcc gcc 432  
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Ser Ala Ser Ala  
130 135 140

cca acc ctt ttc ccc ctc gtc tcc tgt gag aat tcc ccg tcg gat acg 480  
Pro Thr Leu Phe Pro Leu Val Ser Cys Glu Asn Ser Pro Ser Asp Thr  
145 150 155 160

agc agc gtg gcc gtt ggc tgc ctc gca cag gac ttc ctt ccc gac tcc 528  
Ser Ser Val Ala Val Gly Cys Leu Ala Gln Asp Phe Leu Pro Asp Ser  
165 170 175

atc act ttc tcc tgg aaa tac aag aac aac tct gac atc agc agc acc 576  
Ile Thr Phe Ser Trp Lys Tyr Lys Asn Asn Ser Asp Ile Ser Ser Thr  
180 185 190

cgg ggc ttc cca tca gtc ctg aga ggg ggc aag tac gca gcc acc tca	624
Arg Gly Phe Pro Ser Val Leu Arg Gly Gly Lys Tyr Ala Ala Thr Ser	
195 200 205	
cag gtg ctg ctg cct tcc aag gac gtc atg cag ggc aca gac gaa cac	672
Gln Val Leu Leu Pro Ser Lys Asp Val Met Gln Gly Thr Asp Glu His	
210 215 220	
gtg gtg tgc aaa gtc cag cac ccc aac ggc aac aaa gaa aag aac gtg	720
Val Val Cys Lys Val Gln His Pro Asn Gly Asn Lys Glu Lys Asn Val	
225 230 235 240	
cct ctt cca gtg att gct gag ctg cct ccc aaa gtg agc gtc ttc gtc	768
Pro Leu Pro Val Ile Ala Glu Leu Pro Pro Lys Val Ser Val Phe Val	
245 250 255	
cca ccc cgc gac ggc ttc ttc ggc aac ccc cgc aag tcc aag ctc atc	816
Pro Pro Arg Asp Gly Phe Phe Gly Asn Pro Arg Lys Ser Lys Leu Ile	
260 265 270	
tgc cag gcc acg ggt ttc agt ccc cgg cag att cag gtg tcc tgg ctg	864
Cys Gln Ala Thr Gly Phe Ser Pro Arg Gln Ile Gln Val Ser Trp Leu	
275 280 285	
cgc gag ggg aag cag gtg ggg tct ggc gtc acc acg gac cag gtg cag	912
Arg Glu Gly Lys Gln Val Gly Ser Gly Val Thr Thr Asp Gln Val Gln	
290 295 300	
gct gag gcc aaa gag tct ggg ccc acg acc tac aag gtg acc agc aca	960
Ala Glu Ala Lys Glu Ser Gly Pro Thr Thr Tyr Lys Val Thr Ser Thr	
305 310 315 320	
ctg acc atc aaa gag agc gac tgg ctc ggc cag agc atg ttc acc tgc	1008
Leu Thr Ile Lys Glu Ser Asp Trp Leu Gly Gln Ser Met Phe Thr Cys	
325 330 335	
cgc gtg gat cac agg ggc ctg acc ttc cag cag aat gcg tcc tcc atg	1056

Arg Val Asp His Arg Gly Leu Thr Phe Gln Gln Asn Ala Ser Ser Met	
340 345 350	
tgt gtc ccc gat caa gac aca gcc atc cgg gtc ttc gcc atc ccc cca	1104
Cys Val Pro Asp Gln Asp Thr Ala Ile Arg Val Phe Ala Ile Pro Pro	
355 360 365	
tcc ttt gcc agc atc ttc ctc acc aag tcc acc aag ttg acc tgc ctg	1152
Ser Phe Ala Ser Ile Phe Leu Thr Lys Ser Thr Lys Leu Thr Cys Leu	
370 375 380	
gtc aca gac ctg acc acc tat gac agc gtg acc atc tcc tgg acc cgc	1200
Val Thr Asp Leu Thr Thr Tyr Asp Ser Val Thr Ile Ser Trp Thr Arg	
385 390 395 400	
cag aat ggc gaa gct gtg aaa acc cac acc aac atc tcc gag agc cac	1248
Gln Asn Gly Glu Ala Val Lys Thr His Thr Asn Ile Ser Glu Ser His	
405 410 415	
ccc aat gcc act ttc agc gcc gtg ggt gag gcc agc atc tgc gag gat	1296
Pro Asn Ala Thr Phe Ser Ala Val Gly Glu Ala Ser Ile Cys Glu Asp	
420 425 430	
gac tgg aat tcc ggg gag agg ttc acg tgc acc gtg acc cac aca gac	1344
Asp Trp Asn Ser Gly Glu Arg Phe Thr Cys Thr Val Thr His Thr Asp	
435 440 445	
ctg ccc tcg cca ctg aag cag acc atc tcc cgg ccc aag ggg gtg gcc	1392
Leu Pro Ser Pro Leu Lys Gln Thr Ile Ser Arg Pro Lys Gly Val Ala	
450 455 460	
ctg cac agg ccc gat gtc tac ttg ctg cca cca gcc cgg gag cag ctg	1440
Leu His Arg Pro Asp Val Tyr Leu Leu Pro Pro Ala Arg Glu Gln Leu	
465 470 475 480	
aac ctg cgg gag tcg gcc acc atc acg tgc ctg gtg acg ggc ttc tct	1488
Asn Leu Arg Glu Ser Ala Thr Ile Thr Cys Leu Val Thr Gly Phe Ser	

485	490	495	
ccc gcg gac gtc ttc gtg cag tgg atg cag agg ggg cag ccc ttg tcc			1536
Pro Ala Asp Val Phe Val Gln Trp Met Gln Arg Gly Gln Pro Leu Ser			
500	505	510	
ccg gag aag tat gtg acc agc gcc cca atg cct gag ccc cag gcc cca			1584
Pro Glu Lys Tyr Val Thr Ser Ala Pro Met Pro Glu Pro Gln Ala Pro			
515	520	525	
ggc cgg tac ttc gcc cac agc atc ctg acc gtg tcc gaa gag gaa tgg			1632
Gly Arg Tyr Phe Ala His Ser Ile Leu Thr Val Ser Glu Glu Glu Trp			
530	535	540	
aac acg ggg gag acc tac acc tgc gtg gtg gcc cat gag gcc ctg ccc			1680
Asn Thr Gly Glu Thr Tyr Thr Cys Val Val Ala His Glu Ala Leu Pro			
545	550	555	560
aac agg gtc acc gag agg acc gtg gac aag tcc acc ggt aaa ccc acc			1728
Asn Arg Val Thr Glu Arg Thr Val Asp Lys Ser Thr Gly Lys Pro Thr			
565	570	575	
ctg tac aac gtg tcc ctg gtc atg tcc gac aca gct ggc acc tgc tac			1776
Leu Tyr Asn Val Ser Leu Val Met Ser Asp Thr Ala Gly Thr Cys Tyr			
580	585	590	
tga			1779

&lt;210&gt; 2

&lt;211&gt; 592

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2

Met Glu Phe Gly Leu Ser Trp Leu Phe Leu Val Ala Ile Leu Lys Gly

1

5

10

15

Val Gln Cys Glu Val Gln Leu Leu Asp Ser Gly Gly Gly Leu Val Gln  
 20 25 30  
 Pro Gly Gly Cys Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe  
 35 40 45  
 Ser Ser Cys Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu  
 50 55 60  
 Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala  
 65 70 75 80  
 Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Lys Ser Lys Asn  
 85 90 95  
 Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val  
 100 105 110  
 Tyr Tyr Cys Ala Lys Gly Gly Asn Asp Ile Leu Thr Gly Tyr Tyr Ala  
 115 120 125  
 Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Ser Ala Ser Ala  
 130 135 140  
 Pro Thr Leu Phe Pro Leu Val Ser Cys Glu Asn Ser Pro Ser Asp Thr  
 145 150 155 160  
 Ser Ser Val Ala Val Gly Cys Leu Ala Gln Asp Phe Leu Pro Asp Ser  
 165 170 175  
 Ile Thr Phe Ser Trp Lys Tyr Lys Asn Asn Ser Asp Ile Ser Ser Thr  
 180 185 190  
 Arg Gly Phe Pro Ser Val Leu Arg Gly Gly Lys Tyr Ala Ala Thr Ser  
 195 200 205  
 Gln Val Leu Leu Pro Ser Lys Asp Val Met Gln Gly Thr Asp Glu His  
 210 215 220  
 Val Val Cys Lys Val Gln His Pro Asn Gly Asn Lys Glu Lys Asn Val  
 225 230 235 240  
 Pro Leu Pro Val Ile Ala Glu Leu Pro Pro Lys Val Ser Val Phe Val  
 245 250 255  
 Pro Pro Arg Asp Gly Phe Phe Gly Asn Pro Arg Lys Ser Lys Leu Ile  
 260 265 270  
 Cys Gln Ala Thr Gly Phe Ser Pro Arg Gln Ile Gln Val Ser Trp Leu  
 275 280 285  
 Arg Glu Gly Lys Gln Val Gly Ser Gly Val Thr Thr Asp Gln Val Gln  
 290 295 300  
 Ala Glu Ala Lys Glu Ser Gly Pro Thr Thr Tyr Lys Val Thr Ser Thr

305	310	315	320
Leu Thr Ile Lys Glu Ser Asp Trp Leu Gly Gln Ser Met Phe Thr Cys			
325	330	335	
Arg Val Asp His Arg Gly Leu Thr Phe Gln Gln Asn Ala Ser Ser Met			
340	345	350	
Cys Val Pro Asp Gln Asp Thr Ala Ile Arg Val Phe Ala Ile Pro Pro			
355	360	365	
Ser Phe Ala Ser Ile Phe Leu Thr Lys Ser Thr Lys Leu Thr Cys Leu			
370	375	380	
Val Thr Asp Leu Thr Thr Tyr Asp Ser Val Thr Ile Ser Trp Thr Arg			
385	390	395	400
Gln Asn Gly Glu Ala Val Lys Thr His Thr Asn Ile Ser Glu Ser His			
405	410	415	
Pro Asn Ala Thr Phe Ser Ala Val Gly Glu Ala Ser Ile Cys Glu Asp			
420	425	430	
Asp Trp Asn Ser Gly Glu Arg Phe Thr Cys Thr Val Thr His Thr Asp			
435	440	445	
Leu Pro Ser Pro Leu Lys Gln Thr Ile Ser Arg Pro Lys Gly Val Ala			
450	455	460	
Leu His Arg Pro Asp Val Tyr Leu Leu Pro Pro Ala Arg Glu Gln Leu			
465	470	475	480
Asn Leu Arg Glu Ser Ala Thr Ile Thr Cys Leu Val Thr Gly Phe Ser			
485	490	495	
Pro Ala Asp Val Phe Val Gln Trp Met Gln Arg Gly Gln Pro Leu Ser			
500	505	510	
Pro Glu Lys Tyr Val Thr Ser Ala Pro Met Pro Glu Pro Gln Ala Pro			
515	520	525	
Gly Arg Tyr Phe Ala His Ser Ile Leu Thr Val Ser Glu Glu Glu Trp			
530	535	540	
Asn Thr Gly Glu Thr Tyr Thr Cys Val Val Ala His Glu Ala Leu Pro			
545	550	555	560
Asn Arg Val Thr Glu Arg Thr Val Asp Lys Ser Thr Gly Lys Pro Thr			
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Leu Tyr Asn Val Ser Leu Val Met Ser Asp Thr Ala Gly Thr Cys Tyr			
580	585	590	

<210> 3  
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 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)..(723)  
 <223>

<400> 3

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 Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser  
 1 5 10 15

ggt gcc tac ggg gac atc gtg atg acc cag tct cca gac tcc ctg gct 96  
 Gly Ala Tyr Gly Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala  
 20 25 30

gtg tct ctg ggc gag agg gcc acc atc aac tgc aag tcc agc cag agt 144  
 Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser  
 35 40 45

gtt tta tac agc tcc aac aat aag aac tac tta gct tgg tac cag cag 192  
 Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln  
 50 55 60

aaa cca gga cag cct cct aag ctg ctc att tac tgg gca tct acc cgg 240  
 Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg  
 65 70 75 80

gaa tcc ggg gtc cct gac cga ttc agt ggc agc ggg tct ggg aca gat 288  
 Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp  
 85 90 95

ttc act ctc acc atc agc agc ctg cag gct gaa gat gtg gca gtt tat 336  
 Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr



100	105	110	
tac tgt cag caa tat tat agt act cct ccg acg ttc ggc caa ggg acc			384
Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr			
115	120	125	
aag gtg gaa atc aaa cga act gtg gct gca cca tct gtc ttc atc ttc			432
Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe			
130	135	140	
ccg cca tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc			480
Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys			
145	150	155	160
ctg ctg aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg			528
Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val			
165	170	175	
gat aac gcc ctc caa tog ggt aac tcc cag gag agt gtc aca gag cag			576
Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln			
180	185	190	
gac agc aag gac agc acc tac agc ctc agc agc acc ctg acg ctg agc			624
Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser			
195	200	205	
aaa gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat			672
Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His			
210	215	220	
cag ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag tgt			720
Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys			
225	230	235	240
tag			723

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 <212> PRT  
 <213> Homo sapiens

<400> 4

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser  
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 Gly Ala Tyr Gly Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala  
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 Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser  
 35 40 45  
 Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln  
 50 55 60  
 Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg  
 65 70 75 80  
 Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp  
 85 90 95  
 Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr  
 100 105 110  
 Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr  
 115 120 125  
 Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe  
 130 135 140  
 Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys  
 145 150 155 160  
 Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val  
 165 170 175  
 Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln  
 180 185 190  
 Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser  
 195 200 205  
 Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His  
 210 215 220  
 Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
 225 230 235 240

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 <212> DNA  
 <213> Homo sapiens

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 <222> (1)..(480)  
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<400> 5

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 Met Lys Asn His Leu Leu Phe Trp Gly Val Leu Ala Val Phe Ile Lys  
 1 5 10 15

gct gtt cat gtg aaa gcc caa gaa gat gaa agg att gtt ctt gtt gac 96  
 Ala Val His Val Lys Ala Gln Glu Asp Glu Arg Ile Val Leu Val Asp  
 20 25 30

aac aaa tgt aag tgt gcc cgg att act tcc agg atc atc cgt tct tcc 144  
 Asn Lys Cys Lys Cys Ala Arg Ile Thr Ser Arg Ile Ile Arg Ser Ser  
 35 40 45

gaa gat cct aat gag gac att gtg gag aga aac atc cga att att gtt 192  
 Glu Asp Pro Asn Glu Asp Ile Val Glu Arg Asn Ile Arg Ile Ile Val  
 50 55 60

cct ctg aac aac agg gag aat atc tct gat ccc acc tca cca ttg aga 240  
 Pro Leu Asn Asn Arg Glu Asn Ile Ser Asp Pro Thr Ser Pro Leu Arg  
 65 70 75 80

acc aga ttt gtg tac cat ttg tct gac ctc tgt aaa aaa tgt gat cct 288  
 Thr Arg Phe Val Tyr His Leu Ser Asp Leu Cys Lys Lys Cys Asp Pro  
 85 90 95

aca gaa gtg gag ctg gat aat cag ata gtt act gct acc cag agc aat 336

Thr Glu Val Glu Leu Asp Asn Gln Ile Val Thr Ala Thr Gln Ser Asn  
 100 105 110

atc tgt gat gaa gac agt gct aca gag acc tgc tac act tat gac aga 384  
 Ile Cys Asp Glu Asp Ser Ala Thr Glu Thr Cys Tyr Thr Tyr Asp Arg  
 115 120 125

aac aag tgc tac aca gct gtg gtc cca ctc gta tat ggt ggt gag acc 432  
 Asn Lys Cys Tyr Thr Ala Val Val Pro Leu Val Tyr Gly Gly Glu Thr  
 130 135 140

aaa atg gtg gaa aca gcc tta acc cca gat gcc tgc tat cct gac taa 480  
 Lys Met Val Glu Thr Ala Leu Thr Pro Asp Ala Cys Tyr Pro Asp  
 145 150 155

<210> 6

<211> 159

<212> PRT

<213> Homo sapiens

<400> 6

Met Lys Asn His Leu Leu Phe Trp Gly Val Leu Ala Val Phe Ile Lys  
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Ala Val His Val Lys Ala Gln Glu Asp Glu Arg Ile Val Leu Val Asp  
 20 25 30

Asn Lys Cys Lys Cys Ala Arg Ile Thr Ser Arg Ile Ile Arg Ser Ser  
 35 40 45

Glu Asp Pro Asn Glu Asp Ile Val Glu Arg Asn Ile Arg Ile Ile Val  
 50 55 60

Pro Leu Asn Asn Arg Glu Asn Ile Ser Asp Pro Thr Ser Pro Leu Arg  
 65 70 75 80

Thr Arg Phe Val Tyr His Leu Ser Asp Leu Cys Lys Lys Cys Asp Pro  
 85 90 95

Thr Glu Val Glu Leu Asp Asn Gln Ile Val Thr Ala Thr Gln Ser Asn  
 100 105 110

Ile Cys Asp Glu Asp Ser Ala Thr Glu Thr Cys Tyr Thr Tyr Asp Arg

115	120	125
Asn Lys Cys Tyr Thr Ala Val Val Pro Leu Val Tyr Gly Gly Glu Thr		
130	135	140
Lys Met Val Glu Thr Ala Leu Thr Pro Asp Ala Cys Tyr Pro Asp		
145	150	155

<210> 7

<211> 24

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized sequence

<400> 7

ccaacggcaa caaagaaaag aacg

24

<210> 8

<211> 24

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized sequence

<400> 8

aacatgctct ggccgagcca gtcg

24

<210> 9

<211> 24

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized sequence

<400> 9

gcaagtcag ccagagtgtt ttat

24

<210> 10

<211> 24

<212> DNA

<213> Artificial

<220>

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<400> 10

ctgtccttgc tgcctgctc tgtg

24

<210> 11

<211> 33

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized primer sequence

<400> 11

aacagctoga gccaccatgg agtttgggct gag

33

<210> 12

<211> 32

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized primer sequence

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agcggccagc cgccccgagc ctgtcgacag gc

32

<210> 13

<211> 32

<212> DNA

<213> Artificial

<220>

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<400> 13

atagaattcc accatggtgt tgcagaccca gg

32

<210> 14

<211> 30

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized primer sequence

<400> 14

ggagcaggcg gccgcacttc tocctctaac

30

<210> 15

<211> 24

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized sequence

<400> 15

accattgaga accagatttg tgta

24

<210> 16

<211> 24

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized sequence

<400> 16

tgtgtagcac ttgtttctgt cata

24

<210> 17

<211> 28

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized primer sequence

<400> 17

atgaattcca ccatgaagaa ccatttgc

28

<210> 18

<211> 26

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized primer sequence

<400> 18



tatctagatt agtcaggata gcaggc